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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2003, 15:04:29 ; Search time 15.0398 Seconds

(without alignments)
2160.495 Million cell updates/sec

Title: US-09-807-933B-7

Perfect score: 1826

Sequence: 1 MKFTVAITSAVALALSSA.....TFKEVTPALVTRSGCERK 338

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	758.5	41.5	229	2	UC7308 cellulase (EC 3.2.
2	568.5	31.7	511	2	SI0527 endoglucanase B pr
3	525.5	28.8	393	2	SS9499 cellulase eg11 - s
4	233.5	12.8	471	1	A26160 cellulose 1,4-beta
5	233.5	12.8	471	1	A38979 cellulose 1,4-beta
6	198.5	10.9	418	1	S28372 cellulase (EC 3.2.
7	198	10.8	410	1	S68155 cellulase (EC 3.2.
8	181	9.9	438	1	S70602 cellulose 1,4-beta
9	174.5	9.6	533	2	T33912 hypothetical prote
10	169.5	9.3	475	2	S49886 probable membrane
11	159.5	8.7	4776	2	E95206 cell wall surface
12	159	8.7	2395	1	SS0820 surface protein ty
13	156	8.5	605	2	T33913 hypothetical prote
14	155	8.5	1428	2	T08852 luteirin A - Callif
15	153	8.4	503	2	S63257 probable membrane
16	150	8.2	662	2	A45155 mucin FIM-C.1 - Af
17	148.5	8.1	797	1	VCBEX1 glycoprotein X pre
18	148.5	8.1	1275	2	T33369 hypothetical prote
19	148	8.1	402	2	EB6185 hypothetical prote
20	147.5	8.1	463	2	T84444 hypothetical prote
21	147.5	8.1	867	2	T45463 membrane glycoprot
22	147	8.1	542	2	S64030 probable membrane
23	147	8.1	937	2	SS8135 hypothally regulated
24	147	8.1	1777	2	T34369 hypothetical prote
25	146.5	8.0	1032	2	T34433 hypothetical prote
26	146.5	8.0	2232	2	T34434 microfilament shea
27	146	8.0	354	2	T46740 carboxymethylcellu
28	143	7.8	962	2	S03818 mucin-like glycopr
29	143	7.8	1832	2	T31113

30	142	7.8	263	2	S01360 salivary glue prot
31	142	7.8	417	2	UC7092 Paul protein - fis
32	141.5	7.7	888	2	T46726 secreted acid phos
33	141	7.7	556	2	S51892 probable membrane
34	140.5	7.7	329	2	S38082 pathogenesis-relat
35	140	7.7	537	2	B33485 spore coat protein
36	139.5	7.6	720	1	A55160 Trg protein - fru
37	139	7.6	242	2	S60143 cellulase (EC 3.2.
38	139	7.6	304	2	T15922 hypothetical prote
39	139	7.6	344	2	T40167 hypothetical prote
40	139	7.6	748	2	S19652 celldextrinase C
41	139	7.6	786	1	A47547 serine proteinase
42	138.5	7.6	378	2	S61992 sig1 protein - yea
43	138.5	7.6	388	1	UC5461 cellulase (EC 3.2.
44	138.5	7.6	2639	2	T31328 fibroin - Chinese
45	138	7.6	513	1	EUTQI cellulose 1,4-beta

ALIGNMENTS

RESULT 1

UC7308 cellulase (EC 3.2.1.4) - Scopulariopsis brevicaulis

N:Alternate names: endoglucanase I

C:Species: Scopulariopsis brevicaulis

C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000

C:Accession: UC7308; PC7087

R:Nakatsui, F.; Kawaguchi, T.; Takada, G.; Sumitani, J.; Moriyama, Y.; Arai, M.

Biosci. Biotechnol. Biochem. 64, 1238-1246, 2000

A>Title: Cloning and sequencing of an endoglucanase gene from Scopulariopsis brevicaulis

A:Reference number: J7308

A:Accession: UC7308

A:Molecule type: DNA

A:Residues: 1-229 <NAK>

A:Experimental source: strain TOF-1212

A:Accession: PC7087

A:Molecule type: protein

A:Residues: 21-37,149-164 <NA2>

A:Gene: eg1

A:introns: 147/3

C:Keywords: glycosidase; hydrolase

Query Match	Best Local Similarity	Score	DB 2	Length	Matches	Conservative	Mismatches	Indels	Gaps
QY 134	SGSGSTRYWDCCASGSPGKASVT-GPVDTCASNGISLIDAN-AOSGCN-GGNGFMCN	41.5%	62.8%	190	130	30	44	3	3
DB 22	SGGTTRRYWDCCAPSCSWPKAPLSGCPMTCDINPDLDDGLTBSGCPGGAYVCS			81					
QY 191	NNQPAVNDLAYPAAASINAGNCCGCEYLTFTSGAASGKRVVQVNTGGDGS			250					
DB 82	SHSPWAVDDELAAGMAAVNIGQTESDWCACYELEFTGAVSGKMKVQATNTGGDIGN			141					
QY 251	NHPDLQMPGGGVGIFNGCAAGWGA.PNDGWRGARYGVSSVSVCASLPSALQCGKRRPWF			310					
DB 142	NHPIAPMGGVGIFNGCTDQWSPPNGWGRYGVVTRADUCSPPEALKAGCEWRPWF			201					
QY 311	KNSDPTMTFKKVCAPALVTRSGCER 337								
DB 202	GCTDNPVFSFRVECPALVOKSQQR 228								

RESULT 2

SI0527 endoglucanase B precursor - Pseudomonas fluorescens

C:Species: Pseudomonas fluorescens

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 08-Oct-1999

C:Accession: SI0527

R:Gilbert, H.J.; Hall, J.; Hazlewood, G.P.; Ferreira, L.M.A.

Mol. Microbiol. 4, 759-767, 1990

A>Title: The N-terminal region of an endoglucanase from *Pseudomonas fluorescens* subspecies
 A:Reference number: S10527; MUID:90355836; PMID:2117693
 A:Accession: S10527
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-511 <GIL>
 A:Cross-references: EMBL:X52615; NID:945497; PIDN:CAA36844.1; PID:945498
 C:Superfamily: bacterial cellulose-binding domain homology; glycosidase GWM domain hom
 F:31-128/Domain: bacterial cellulose-binding domain homology <BCB>
 F:180-217/Domain: glycosidase GWM domain homology <GWS>
 F:32-137/Disulfide bonds: #status predicted

Query Match 31.1%; Score 568.5; DB 2; Length 511;
 Best Local Similarity 33.4%; Pred. No. 26-29;
 Matches 136; Conservative 60; Mismatches 126; Indels 85; Gaps 13;

QY 8 TSIAVALALSSAEAAACSSVYGO-CGGIGMSGPTCCESG-----TCVAQEGNKYYSQ 60
 DB 102 SSVRGVQGNNGSSRAQVPAVTGATCGGSSAPSSVSSSSSVSTPRSSSSSVSS 161
 QY 61 CLPGSHS-----NNAAGNASTKTKSTTKSTTTAKAT---AT 93
 DB 162 SVPGTSSSSSVLTGAQACNMYGTLPPLCNMTSGMGYEDGRSCVARTTCSAQAPAYGI 221
 QY 94 VTTKYVTKTKTKTKTKST-----TAASTTSSAGKVIYSGKSGSGSTRYMPDCK 147
 DB 222 VETSSSTPLSSSSSSSVSSSSLSATSSASVSVPPIDGG--CNGYATRYMDCCK 219
 QY 148 ASGSMPEKA-SYTGFPVDTCAANGISILDANAQSGCNGMGFNNQPMAYNDELAYGA 206
 DB 280 PHCGSANVPISVPSLOCSANNTRLSDVSGSCGGGGYCMWKIPFAVSPILAYGA 339
 QY 207 AASIASNEAGWCCG-CYELTF-----SGAAGKMYVQVNTGDLGSHFP 254
 DB 340 AYS-----SGDVCGRCYQLOFTGSSYNAPGPDGSAALAKMTIYDANIVDVSQGF 393
 QY 255 LMPGGGAGIENGCAQMGAPNDGMRGYSV-----SSVSD-----CASL 295
 DB 394 ILVPGGVGAFNACSAQMGVSNALGQYGFLLAACKQOLGYNASLSQYKSCVLRCDVS 453
 QY 296 -----PSALQACKRFNFWFNSNPTMTFKEVTCPAELTTRSGER 337
 DB 454 FSGRLTLOQSCWTFEMFPAADPSLKYKEVPCPAELTTRSGMR 500

RESULT 3

559499 cellulase egII - smut fungus (Ustilago maydis)
 C:Species: Ustilago maydis (corn smut)
 C>Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 28-May-1999
 C:Accession: S59499
 R:Schumacher, F.; Wanner, G.; Kahmann, R.
 Biol. Chem. Hoppe-Seyler 376, 617-625, 1995
 A>Title: Filament-specific expression of a cellulase gene in the dimorphic fungus *Ustilago*
 A:Reference number: S59499; MUID:96145720; PMID:8590631
 A:Accession: S59499
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-393 <SCF>
 A:Cross-references: GB:S81598; NID:g1478378; PIDN:AAA36147.1; PID:g1478379

Query Match 28.8%; Score 525.5; DB 2; Length 393;
 Best Local Similarity 48.6%; Pred. No. 9.1e-77;
 Matches 107; Conservative 28; Mismatches 60; Indels 25; Gaps 10;

QY 136 SSGSTRYWDCKKASGMPGKAVTGVPVDTCAANGISILDAA-----NAQSGCNGMGFNN 191
 DB 26 AGMAYRYWDCCLASAWGKAPVYAPVDAKADGVLIDSKDPGSGCGKNGKFKCSC 85
 QY 192 NQPMVNDP-----LAYGAAASIASNEAGWCCGCELTFTSGAASGK-----GMVQV 242
 DB 86 MDPF--DDEPTPLAFGGA--FTTQGESDTCACVYAFEND--AGGAMAMKMLIQT 140

QY 243 NMGDLGSHNFDLQPGGVGIF-NGCAQMGAPNDGMRGYSVSDCASPSALQA 301
 DB 141 NVGADVQSNFDFOLPGGGLGAFPKGCPQMGVBSLMDQYGGVKSATFECSKLPLOE 200
 QY 302 GCKMRFPN-WFKNSDNPFM--TFKEVTCPAELTTRSGCERK 338
 DB 201 GCKMRFPN--GDMPLKSGPKRVKCPKSLIDRSQCRK 237

RESULT 4

A26160 cellulose 1,4-beta-cellulobiosidase (EC 3.2.1.91) II precursor - fungus (*Trichoderma reesei*)
 N:Alternate names: exo-cellulobiohydrolase II
 C:Species: *Trichoderma reesei*
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A26160; A26472
 R:Chen, C.M.; Gitzalis, M.; Stafford, D.W.
 Bio/Technology 5, 274-278, 1987
 A>Title: Nucleotide sequence and deduced primary structure of cellulohydrolase II from
 A:Reference number: A26160
 A:Accession: A26160
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-471 <CHB>
 R:Reier, T.T.; Lehtovaara, P.; Kauppinen, S.; Salomoni, I.; Knowles, J.
 Gene 51, 43-52, 1987
 A>Title: Homologous domains in *Trichoderma reesei* cellulolytic enzymes: gene sequence and
 A:Reference number: A26472; MUID:87248061; PMID:3596237
 A:Accession: A26472
 A:Molecule type: DNA
 A:Residues: 1-471 <TEB>
 A:Cross-references: GB:M16190; NID:g170540; PIDN:AAA4210.1; PID:g170541
 C:Genetics:
 A:Insertions: 31/2; 160/2; 243/2
 A:Superfamily: cellulose 1,4-beta-cellulobiosidase II; fungal cellulose-binding domain hom
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:31-62/Domain: fungal cellulose-binding domain homology <FCB>

Query Match 12.8%; Score 233.5; DB 1; Length 471;
 Best Local Similarity 37.4%; Pred. No. 5.7e-08;
 Matches 64; Conservative 24; Mismatches 46; Indels 37; Gaps 8;

QY 7 TSIAVALALSSA---EASCSVYGOCCGIGMSGPTCCESGTCVAQEGNKYYSOCLP 63
 DB 6 LTTLATLTLAAVPLEBROKCSVWGQCGQWWSGPTCCASGSTCV--YENDYSSQCLP 63
 QY 64 GSHNNAAGNASTTKTKSTTKSTTTAKATATVTKYVTKTKTKTKT---STAAASTS 119
 DB 64 GA-----ASSSSTRAAS-----TTSKVSPTTSRSSSATPPPGSTTRVPPV 105
 QY 120 TSSSAGYKVISGKSGSGST---TRYWDCKKASGMPGKAVTGVPVDTCA 167
 DB 106 GSGTATY---SGNPFVGVTPMANAYASVBSLAP--SLTGAMATYAA 149

RESULT 5

A38979 cellulose 1,4-beta-cellulobiosidase (EC 3.2.1.91) II - fungus (*Trichoderma viride*)
 C:Species: *Trichoderma viride*
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A38979
 R:Mang, J.R.; Zhang, M.F.; Huang, T.
 Acta Genet. Sin. 22, 74-80, 1995
 A>Title: The primary structure of cellulohydrolase gene (CBH II) from *Trichoderma viride*
 A:Reference number: A38979
 A:Accession: A38979
 A:Molecule type: DNA
 A:Residues: 1-471 <WAN>
 C:Genetics:
 A:Insertions: 31/2; 160/2; 243/1
 C:Superfamily: cellulose 1,4-beta-cellulobiosidase II; fungal cellulose-binding domain hom
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Db 161 DSNNFGKEQVGSGLSLSGAYCIVDHNRYARNNGGVIGGGFTD 204

A:Reference number: A95000; MUID:21357209; PMID:11463916
 A:Accession: R95206
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-4776 <CUR>
 A:Cross-references: GB:AE005672; PIDN:AAK75846.1; PID:G14973269; GSPDB:GN00164; TIGR:SP4
 A:Experimental source: strain TIGR4
 C:Genetics:
 A:Gene: SPI772

Query Match 8.7%; Score 159.5; DB 2; Length 4776;
 Best Local Similarity 25.2%; Pred. No. 0.026;
 Matches 71; Conservative 36; Mismatches 118; Indels 57; Gaps 8;

6 AITSIATVALSSASBAASCSVYGGCGIGMSGPTCCSGSPCAQEGNKYVQCLPGS 65
 DB 4527 ASTSASVSASTSASASTSASASTSASASTSASASTSASASTSASASTSASASTS 4586
 QY 66 HSNNAAG-NASSTKTKTSTTTAKATATVTTKTTTCTTTAASTSTSSA 124
 DB 4587 ASASASISASBASASTSASASTS-ASASASTSASASTSASASTSASASTSASA 4645
 QY 125 GYKVISGKSGSGSTTRYWDCCKASCMPGKASVTGPVDTGASNGISILDANAGCGNCG 184
 DB 4646 S---ASTSASASTS---ASASASTSASASTSASASTSASASTSAS---ASASTSAS-- 4692
 QY 185 NGPFMNNQPMVAUNDELAYGPAASIASGNSAGKCCGCELTFTTSGAASGKMYVQVNT 244
 DB 4693 -----ASASTSASASTSASASTSASASTSVSNANHSNS--QVGN 4729
 QY 245 GGDLSNHFPLQMPGGVGFNPGCAQWAPNDMGARYGV 286
 DB 4730 GSGTGSOKEL-----PNTGTSSIGSV 4752

RESULT 12
 S50820
 Surface protein type 51B - Paramedium tetraurelia
 C:Species: Paramedium tetraurelia
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 07-Dec-1999
 C:Accession: S50820
 R:Scott, J.; Leeck, C.; Forney, J.
 Nucleic Acids Res. 22, 5079-5084, 1994
 A:Title: Analysis of the micronuclear B type surface protein gene in Paramedium tetraurelia
 A:Reference number: S50820; MUID:95096630; PMID:7800503
 A:Accession: S50820
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-2395 <SCO>
 A:Cross-references: EMBL:U07603; NID:G467226; PIDN:AA81947.1; PID:G467227
 C:Genetics:
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1994
 A:Genetic code: GCG5
 A:introns: 472/3; 1310/3; 1821/3
 C:Superfamily: G surface protein

Query Match 8.7%; Score 159; DB 1; Length 2395;
 Best Local Similarity 23.3%; Pred. No. 0.015;
 Matches 89; Conservative 37; Mismatches 152; Indels 104; Gaps 21;

16 LSSASBAASCSVYGGCGIGMSGPTCC-----SGSTCV---AQEGNK----- 56
 DB 1948 VNSDGSKACPR-YTCKSLMNSPTCKMISNOCTTNGSNCIG:TTLCSEYNTDGGCVSG 2006
 QY 57 YYSOCLPESHNNAGNASTKTKSTTTAKATATVTTKTTTCTTTAASTSTSSA 116
 DB 2007 YDAGCI---QSVPLMNSDPKVCCKPYTSC---ADAFYTHSDCQTASKCTCTNGTTCI 2059
 QY 117 STSTSSS-----AGKVISGKSGSGSTTRYWDCCKASGMPGKASVTG----- 160
 DB 2060 ALGACSSYTTGACGVFNDKGLALTSGLTSTGICL--WDYASGCRDSCADLTGTHAT 2117
 QY 161 ---PVDTCASNGISILDANA-----QSGCN---GSGNFGMC-----NNNQPMVA----- 196

DB 2118 CSSQLSTCTSDGTSCLVKGACTSVTTOFACTTAVGSDG-ICVYELASTNNNTAKCRLLA 2176
 QY 197 ---VNDELAYGPAASIASGNSAGNEMWC-----GCYEL---FTSGAASGKMYVQVNTG 245
 DB 2177 CADIQNSTSTNVCAVALSSCVSNAGTACIACANSCSTYTTKTACNSGGIDGICVFQSTATG 2236
 QY 246 GDLGSNHFPLQMPGGVGFNPGC-----AAQMGAPNDMGARYG-GVSSV-SDCA-- 293
 DB 2237 AAGT-----GTCLMTACTTANSDDVACQAAADRCSMTAASGTGTTAVASKCATH 2287
 QY 294 -SLPSALQAGCKWRFPNPS 313
 DB 2288 TCATNQATNGACTRFLNMDKKT 2309

RESULT 13
 T33913
 Hypothetical protein Y25C1A.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T33913
 R:Kalicki, J.; Smith, A.; Gibson, A.
 submitted to the EMBL Data Library, February 1999
 A:Description: The sequence of C. elegans cosmid Y25C1A.
 A:Reference number: Z21437
 A:Accession: T33913
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-605 <KAL>
 A:Cross-references: EMBL:AF125459; PIDN:AAJ12833.1; GSPDB:GN00020; CESP:Y25C1A.3
 A:Experimental source: strain Bristol N2; clone Y25C1A
 C:Genetics:
 A:Gene: CESP:Y25C1A.3
 A:Map position: 2
 A:introns: 392/3; 429/1; 567/3

Query Match 8.5%; Score 156; DB 2; Length 605;
 Best Local Similarity 21.7%; Pred. No. 0.0067;
 Matches 93; Conservative 37; Mismatches 183; Indels 116; Gaps 14;

4 TVALTSIAVALSSASBAASCSVYGGCGIGMSGPTCCSGSTCVAAQEGNKYSQCLP 63
 DB 190 TAAAGSTATTAAAGSTATAAGSTATAAGSTATAAGSTATAAGSTATAAG 247
 QY 64 GS-HSNNAAGNASTKTKSTTTAKATATVTTKTTTCTTTAASTSTSS 122
 DB 248 GSTASTAAGSTATTAAAGSTATTAAAGSTATTAAAGSTATTAAAGSTATTAAAGSTAST 307
 QY 123 SAGKVISGKSGSGSTTRYWDC-----CKASGMPGKASVTGPVDTGASNGISILD 174
 DB 308 AAGGSTATTAAAGSTATTAAAGSTATTAAAGSTATTAAAGSTATTAAAGSTATTAAAGSTAST 367
 QY 175 ANA-QSGCNGGNGMGFCNNQPMVAUNDELAYGFPA----- 207
 DB 368 SPAPAAACEPEYKRFNRPSPGWCIKVFTGY-FAAQIDBRACQAAAGALTLQNDDEALY 426
 QY 208 -----ASIASGNEAGKCCGCELTFTTSGAASGKMYV---Q 240
 DB 427 IQSSILSLQIKOPASAVWIGIKRKASCVGKPDATCTQTOSFEWTDSDGVNAGVFFQKQ 486
 QY 241 VTNNGSL-----GSNHFPLQMPGGVGFNPGCAQWAPNDMGARY 283
 DB 487 PDNGKALNDDCALLASRPTTIAAGTYTAQMBD-----VNCIAFTFAANA--ARKT 538
 QY 284 GGVSSVSDCASLPALQAGCKWRFPNPSDNP-----MTEKEVTCPEAL 329
 DB 539 GGVA-----CGQQPFTCPG--WKF-----FDRPTGCMKVFGTGPHEVQADAEKACQAVG 587
 QY 330 TTRSGCERK 338
 DB 588 ATLSIOHK 596

